

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: LI, Yi and RUBEN, Steven M.

(ii) TITLE OF INVENTION: HUMAN AMINE RECEPTOR POLYPEPTIDES

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

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- (D) STATE: DC
- (E) COUNTRY: UNITED STATES OF AMERICA
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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/314,006
- (B) FILING DATE: 19-MAY-1999
- (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/467,559
- (B) FILING DATE: 06-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: STEFFE, ERIC K
- (B) REGISTRATION NUMBER: 36,688
- (C) REFERENCE/DOCKET NUMBER: 1488.0840001/EKS/HCC

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS

09986745-12001
cm, f

CTAGAGCTAG	CAGGAGTAAC	TCTCATGGAA	CCTTGGAAAC	CATTCTTCAA	TTGAATTTCA		60
GGGCACATTT	GAATCAGTAC	CCAGGGGCAC	TGTACTATGC	TCCCAGCTGG	ACCTTAGTTT		120
CCTCCTCCTC	GTTTCACCCT	GTGAGTAATT	AACAGACAAA	ATTTTTTTTT	TTTTTTTTTT		180
TTTTTTTTTT	TTTTTGCCCT	CCAGTGGAGA	AGGTGGCCAG	TTCTCAGACA	GAGGAAGAGT		240
AGAAATCATA	A ATG AGA GCT GTC TTC ATC CAA GGT GCT GAA GAG CAC CCT						290
	Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro						
	1		5		10		
GCG GCA TTC TGC TAC CAG GTG AAT GGG TCT TGC CCC AGG ACA GTA CAT							338
Ala Ala Phe Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His							
	15		20		25		
ACT CTG GGC ATC CAG TTG GTC ATC TAC CTG ACC TGT GCA GCA GGC ATG							386
Thr Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met							
	30		35		40		45
CTG ATT ATC GTG CTA GGG AAT GTA TTT GTG GCA TTT GCT GTG TCC TAC							434
Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr							
		50			55		60
TTC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC TCC CTG GCC							482
Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala							
		65			70		75
CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTG CCC CTC AGC ACC ATT							530
Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile							
		80			85		90
CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG							578
Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu							
	95				100		105
CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC							626
His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu							
	110				115		120
TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC							674
Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu							
		130					135
TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA							722
Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala							
		145					150
GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT							770
Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp							
	160						165

GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG 818
Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val
175 180 185

GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC 866
Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe
190 195 200 205

CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG 914
Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys
210 215 220

ATC TTT GTG GTT GCT ACC AGA CAG GCT CAG CAG ATT ACC ACA TTG AGC 962
Ile Phe Val Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser
225 230 235

AAA AGC CTG GCT GGG GCT GCC AAG CAT GAG ACA AAA GCT GCC AAG ACC 1010
Lys Ser Leu Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr
240 245 250

CTG GGC ATT GTT GTG GGC ATA TAC CTC TTG TGC TGG CTG CCC TTC ACC 1058
Leu Gly Ile Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr
255 260 265

ATA GAC ACG ATG GTC GAC AGC CTC CTT CAC TTT ATC ACA CCC CCA CTG 1106
Ile Asp Thr Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu
270 275 280 285

GTC TTT GAC ATC TTT ATC TGG TTT GCT TAC TTC AAC TCA GCC TGC AAC 1154
Val Phe Asp Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn
290 295 300

CCC ATC ATC TAT GTC TTT TCC TAC CAG TGG TTT CGG AAG GCA CTG AAA 1202
Pro Ile Ile Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys
305 310 315

CTC ACA CTG AGC CAG AAG GTC TTC TCA CCG CAG ACA CGC ACT GTT GAT 1250
Leu Thr Leu Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp
320 325 330

TTG TAC CAA GAA TGATTCCTTC TACTAAATGC AGGCAAGGAG TAGGACCTCA 1302
Leu Tyr Gln Glu
335

CAGGAAAGAT AAGTGGCACT GTGACCGCGG GCTGTGTGGT GTTGAGTTTG TGGGCATGCT 1362

TCCAGGACAG CATGGGTT 1380

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro Ala Ala Phe
1 5 10 15

Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His Thr Leu Gly
20 25 30

Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met Leu Ile Ile
35 40 45

Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr Phe Lys Ala
50 55 60

Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala Leu Ala Asp
65 70 75 80

Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile Arg Ser Val
85 90 95

Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu His Thr Tyr
100 105 110

Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu Cys Phe Ile
115 120 125

Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu Tyr Pro Ser
130 135 140

Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala Gly Trp Gly
145 150 155 160

Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp Val Val Glu
165 170 175

Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val Gly Ser Cys
180 185 190

Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe Pro Leu Phe
195 200 205

Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys Ile Phe Val
210 215 220

Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser Lys Ser Leu
225 230 235 240

Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile
245 250 255

Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr Ile Asp Thr
260 265 270

Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu Val Phe Asp
275 280 285

Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn Pro Ile Ile

A12
can it
5428860
12001

290 295 300
Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys Leu Thr Leu
305 310 315 320
Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp Leu Tyr Gln
325 330 335
Glu

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGAATTCCT UATGAGAGCT GTCTTCATC

29

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGCTTC GTCATTCTTG GTACAAATCA AC

32

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

A12
cm
0900045 12004
T002T 51200600

30

(D) TOPOLOGY: linear

29

(D) TOPOLOGY: linear

34

(D) TOPOLOGY: linear

60

61

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Arg Leu Leu Val Leu Ala Ser Pro Pro Ala Ser Leu Leu Pro Pro
1 5 10 15
Ala Ser Glu Gly Ser Ala Pro Leu Ser Gln Gln Trp Thr Ala Gly Met
20 25 30
Gly Leu Leu Val Ala Leu Ile Val Leu Leu Ile Val Val Gly Asn Val
35 40 45
Leu Val Ile Val Ala Ile Ala Lys Thr Pro Arg Leu Gln Thr Leu Thr
50 55 60
Asn Leu Phe Ile Met Ser Leu Ala Ser Ala Asp Leu Val Met Gly Leu
65 70 75 80
Leu Val Val Pro Phe Gly Ala Thr Ile Val Val Trp Gly Arg Trp Glu
85 90 95
Tyr Gly Ser Phe Phe Cys Glu Leu Trp Thr Ser Val Asp Val Leu Cys
100 105 110
Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala Leu Asp Arg Tyr
115 120 125
Leu Ala Ile Thr Ser Pro Phe Arg Tyr Gln Ser Leu Leu Thr Arg Ala
130 135 140
Arg Ala Arg Ala Leu Val Cys Thr Val Trp Ala Ile Ser Ala Leu Val
145 150 155 160
Ser Phe Leu Pro Ile Leu Met His Trp Trp Arg Ala Glu Ser Asp Glu
165 170 175
Ala Arg Arg Cys Tyr Asn Asp Pro Lys Cys Cys Asp Phe Val Thr Asn
180 185 190
Arg Ala Tyr Ala Ile Ala Ser Ser Val Val Ser Phe Tyr Val Pro Leu
195 200 205
Cys Ile Met Ala Phe Val Tyr Leu Arg Val Phe Arg Glu Ala Gln Lys
210 215 220

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cm

Gln Val Lys Lys Ile Asp Ser Cys Glu Arg Arg Phe Leu Gly Gly Pro
225 230 235 240

Ala Arg Pro Pro Ser Pro Glu Pro Ser Pro Ser Pro Gly Pro Pro Arg
245 250 255

Pro Ala Asp Ser Leu Ala Asn Gly Arg Ser Ser Lys Arg Arg Pro Ser
260 265 270

Arg Leu Val Ala Leu Arg Glu Gln Lys Ala Leu Lys Thr Leu Gly Ile
275 280 285

Ile Met Gly Val Phe Thr Leu Cys Trp Leu Pro Phe Phe Leu Ala Asn
290 295 300

Val Val Lys Ala Phe His Arg Asp Leu Val Pro Asp Arg Leu Phe Val
305 310 315 320

Phe Phe Asn Trp Leu Gly Tyr Ala Asn Ser Ala Phe Asn Pro Ile Ile
325 330 335

Tyr Cys Arg Ser Pro Asp Phe Arg Lys Ala Phe Gln Arg Leu Leu Cys
340 345 350

Cys Ala Arg Arg Ala Ala Cys Arg Arg Arg Ala Ala His
355 360 365

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Asp Asp Leu Glu Arg Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser
1 5 10 15

Asp Gly Lys Ala Asp Arg Pro His Tyr Asn Tyr Tyr Ala Thr Leu Leu
20 25 30

Thr Leu Leu Ile Ala Val Ile Val Phe Gly Asn Val Leu Val Cys Met
35 40 45

Ala Val Ser Arg Glu Lys Ala Leu Gln Thr Thr Thr Asn Tyr Leu Ile
50 55 60

Val Ser Leu Ala Val Ala Asp Leu Leu Val Ala Thr Leu Val Met Pro
65 70 75 80

A12
Cm
00000745-112004

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